

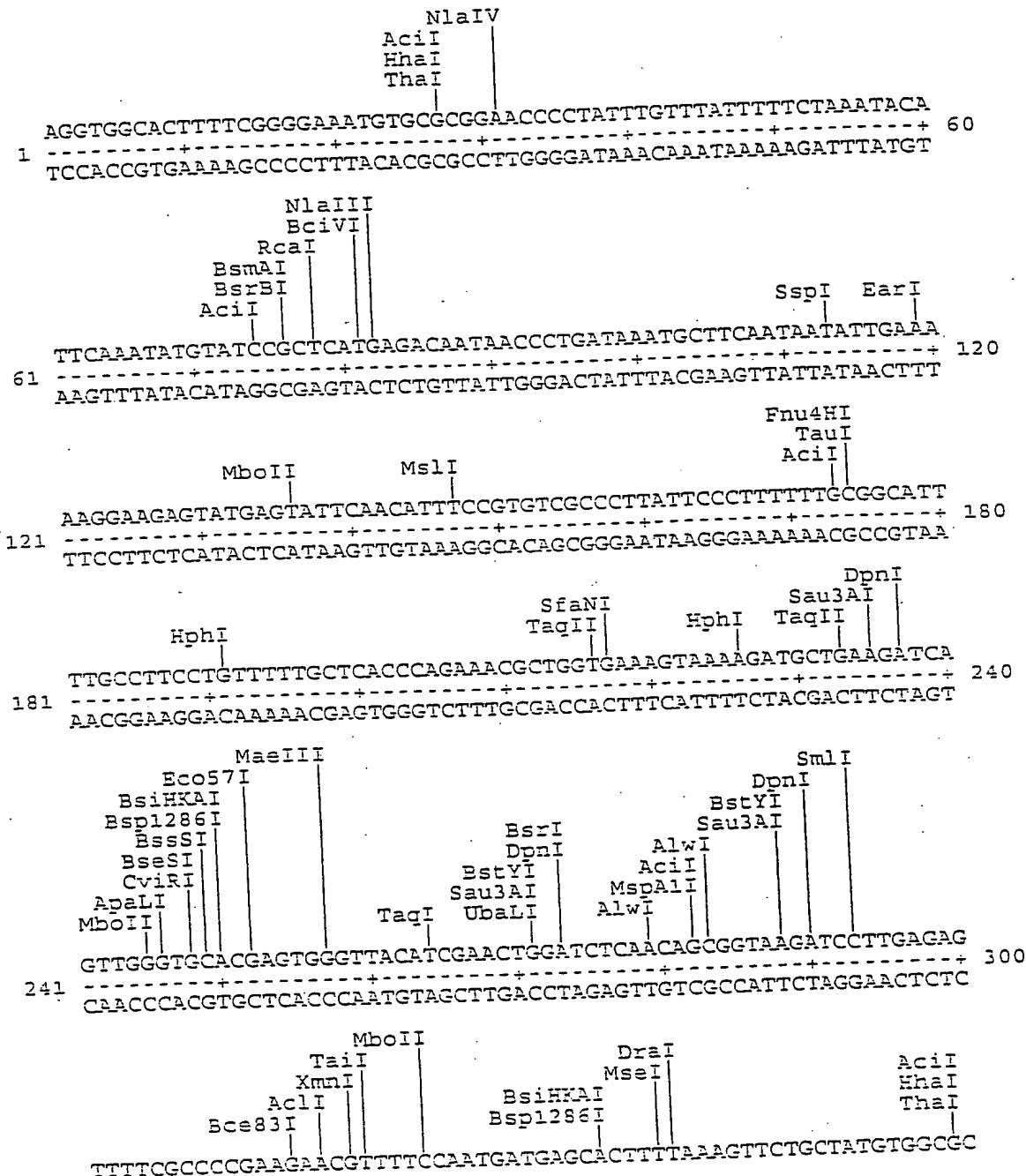


1/21

REPLACEMENT SHEET

Fig. 1A

Restriction map of plasmid ms23





## 2/21 REPLACEMENT SHEET

Fig. 1A (cont.)

301 AAAAGCGGGCTTCTTGCAAAAGGTTACTACTCGTGA<sup>360</sup>  
 361 GGTATTATCCGTATTGACGCCGGCAAGAGCAACTCGTCGCCGATACACTATTCTCA  
 361 CCATAATAGGGATAACTGCGCCGTTCTCGTTGAGCCAGCGGTATGTGATAAGAGT<sup>420</sup>  
 421 GAATGACTTGGTTGAGTACTCACCACTCACAGTACAGAAAAGCATCTTACGGATGGCATGACAGT  
 421 CTTACTGAACCAACTCATGAGTGGTCAGTGTCTTCGTAGAATGCCTACCGTACTGTCA<sup>480</sup>  
 481 AAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGCCAACTTACTTCT  
 481 TTCTCTTAATACGTCACGACGGTATTGGTACTCACTATTGTGACGCCGGTTGAATGAAGA<sup>540</sup>  
 541 GACAACGATCGGAGGACCGAAGGGAGCTAACCGCTTTTGACAAACATGGGGATCATGT  
 541 CTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCGAAAAACGTGTTGACCCCTAGTACA<sup>600</sup>  
 601 AACTCGCCTTGATGTTGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGA  
 601 TTGAGCGGAACTAGCAACCCCTGGCTCGACTTACTTCGGTATGGTTGCTGCTCGCACT<sup>660</sup>  
 661 CACCACGATGCCTGTAGCAATGGCAACAAACGTTGCGCAAACATTTAACTGGCGAACTACT  
 661 GTGGTGCTACGGACATCGTTACCGTTGCAACCGCTTGTATAATTGACCGCTTGATGA<sup>720</sup>  
 661 MseI

HhaI  
FspI  
TaiI  
MseI  
BsrI



JAN 31 2005

3/21

## REPLACEMENT SHEET

Fig.14(cont.)

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721

VspI Tsp509I BccI AvaiI  
AluI MspI CviJI NciI BsrI EcII Sau96I  
BfaI ScrFI MnII AcII FokI CviRI  
TACTCTAGCTCCCGGCAACAATTAATAGACTGGATGGAGCCGGATAAGTTGCAGGACC  
ATGAGATCGAAGGGCCGTTGTTAATTATCTGACCTACCTCCGCCTATTCACGTCCTGG 780

781

CviJI Cac8I MspI  
CviJI HaeIII BglI BsrFI  
Sau96I MspI CviJI  
HhaI MwoI NlaIV  
ACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTATTGCTGATAATCTGGAGCCGGTGA  
TGAAGACCGAGCCGGAGGCCGACCGACCAAATAACGACTATTTAGACCTCGGCCACT 840

841

AciI BccI  
BsaI BfiI  
BsmAI BbvI  
ThaI CviJI  
BpmI HaeIII  
HphI Fnu4HI Bsrl  
SimI CviRI TspRI  
Hin4I BsrDI TseI Sau96I CviJI BscGI MnII  
GGTGGGTCTCGCGGTATCATTGCAGCACTGGGCCAGATGGTAAGCCCTCCGTATCGT  
CGCACCCAGAGCGCCATAGTAACGTGACCCGGTCTACCATTGGGAGGGCATAGCA 900

901

HinfI BseMII  
AhdI HaeIV  
HaeIV BscGI PleI Sau3AI DpnI  
Hin4I BscGI FokI DdeI  
AGTTATCTACAGACGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGA  
TCAATAGATGTGCTGCCCTCAGTCCGTTGATACTACTTGCTTATCTGTCTAGCGACT 960

961

NlaIV MnII Bst4CI DpnI  
BaiI MspI CjePI BstYI  
TspRI MaeIII Sau3AI  
GATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTACTCATATATACT  
CTATCCACGGAGTGACTAATTGTAACCATTGACAGTCTGGTCAATTGAGTATATG 1020

021

DraI Tsp509I DpnI BstYI Sau3AI  
CjePI MspI MspI MspI AlwI  
MspI DpnI BstYI Sau3AI AlwI  
TTAGATTGATTAACTTCATTAAATTAAAAGGATCTAGGTGAAGATCCTTTTGA  
AATCTAACTAAATTGAAAGTAAAATTAAATTTCCTAGATCCACTCTAGGAAAPCT 1080



JAN 31 2005

4/21 REPLACEMENT SHEET

Fig. 1A (cont.)

1081	UbaLI	Bsp24I	CjePI	CjeI	TspRI	BseMII	DdeI	SmaI	BscGI
	NlaIII	RcaI	MseI	TaiI					
	<pre> TAATCTCATGACCAAAATCCCTAACGTGAGTTTCGTTCCACTGAGCGTCAGACCCCGT ATTAGAGTACTGGTTTAGGAAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCA </pre>								
	1140								

Shy T



Fig.1A(cont.)

5/21 REPLACEMENT SHEET

1441 AAGACGATAGTTACGGATAAGGCAGCGGTCGGCTGAAACGGGGGGTTCGTGCACACA  
 BsiEI CviJI  
 MspI Fnu4HI HhaI TseI BscGI ApaLI  
 BsaWI MaeIII  
 BsiHKAI Bsp1286I BseSI CviRI  
 1500 TTCTGCTATCAATGGCCTATTCCCGCTGCCAGCCCAGCTGCCCCCAAGCACGTGTGT  
 1501 GCCCAGCTTGGAGCGAACGACCTACACCGAACCTGAGATAACCTACAGCGTGAGCATTGAGA  
 BseMII DdeI SfcI  
 CviJI AluI  
 1560 CGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCCACTCGTAACCTCT  
 1561 AAGGCCACGCTTCCCAGGGAGAAAGGCGGACAGGTATCCGTAAGCGGCAGGGTCGG  
 Fnu4HI TauI  
 HaeII HhaI EciI BsaWI MspI AcIi BcIVI BsI  
 1620 TTCGGTGCAGGGCTTCCCTCTTCCGCTGTCCATAGGCCATTGGCCGTCCCCAGCC  
 1621 AACAGGAGAGCGCACGAGGGAGCTTCAGGGAAACGCCCTGGTATCTTATAGCCTGT  
 ScrFI BsaJI  
 BssSI HhaI AluI CviJI EcoRII  
 MnI EcoRII ScrFI  
 1680 TTGTCCTCTCGCGTGTCCCTCGAAGGTCCCCCTTGGGACCATAGAAATATCAGGACA  
 1681 CGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTGTGATGCTCGTCAGGGGGCGGAG  
 CviJI NlaIV  
 DrdI MnI SfaNI Bce83I EciI AcII  
 HgaI SmlI TaqI  
 1740 GCCCAAAGCGGTGGAGACTGAACTCGAGCTAAACACTACGAGCAGTCCCCCGCCTC  
 1741 CCTATGGAACGCCAGCAACGGGCTTTTACGGTTCTGGCTTTGCTGGCCTT  
 GGTACCTTTGCGGTGTTGCCCGGAAATGCCAAGGACCGGAAACGACCGGAAA  
 NlaIII CviJI HaeI  
 CjeI Fnu4HI TauI HaeIII  
 HaeIII CjeI  
 1800 Bst4CI BsI CviJI HaeI  
 MwoI Cac8I Bst4CI NlaIV  
 Cac8I BsI HaeIII  
 1860 TGCTCACATGTTCTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTT  
 NspI AflIII BspLU111 HinFI TfiI Bst4CI AceIII  
 1850



Fig.1A (cont.)

6/21 REPLACEMENT SHEET

ACGAGTGTCACAGGAAAGGACGCTATAGGGGACTAAGACACCTATTGGCATATAATGGCGGAA

CviJI

1861 TGAGTGAGCTGATAACCGCTCGCCGAGCCGAACGACCGAGCCAGCCAGTCAGTGAGCGA  
 ACTCACTCGACTATCGCGAGCCGCGTCGGCTTGCTGGCTCGCGTCGCTCAGTCAGTCAGTGAGCGA 1920

1921 - - - + - - - + - - - + - - - + - - - + 1980  
CCTTCGGCTTCTCGCGGGTTATGCCGTTTGGCGGAGAGGGGGCGCGCAGCCGGCTAAGTAAAT

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7/21

Fig.1A(cont.)

JAN 3 1 2005



1981 ATGcagcGGATCAAGCTTGGATCCATCGATGAATTGGCGGCCACTAGTGCCTGGCTGC  
 2040 TACgtcgCCTAGTTCGAACCTAGGTAGCTACTTAAGCCGGCGGTGATCACGGCCGGACG

1981 ATGCTAGAGTCGACCGCAAGACCCCTTCCTCTATATAAGGAAGTTCAATTGAGAG  
 2040 TCAGATCTCAGCTGGCGTTCTGGGAAGGAGATATATTCTTCAGTAAAGTAAACCTCTC

2040 GACACGGCTCGAGTGGCCACCATGGTCGTCCTGTAGAAAAACCCCAACCGTGAAATCAAAA  
 2160 CTGTGCGAGCTACCGGTGGTACCAAGGAGACATCTTGGGTTGGGACTTTAGTTT

2160 AACTCGACGGCTGTGGGATTCACTCTGGATCGCGAAAAACTGTGGATTGATCAGCGTT



Fig. 1A (cont.)

8/21 REPLACEMENT SHEET

2161 TTGAGCTGCCGGACACCCGTAAGTCAGACCTAGCGCTTTGACACCTTAACTAGTCGCAA 2220

CjePI	MaeIII	HhaI	ThaI	MunI	Tsp509I	NciI	ScrFI	MspI	CviJI	EcoRII	ScrFI	EcoRII	Sau3AI	MseI	SfaNI	DpnI
-------	--------	------	------	------	---------	------	-------	------	-------	--------	-------	--------	--------	------	-------	------

GGTGGGAAAGCGCGTTACAAGAAAGCCGGGCAATTGCTGTGCCAGGCAGTTAACGATC 2280

2221 CCACCCCTTCGCGCAATGTTCTTCGGCCCGTTAACGACACGGTCCGTCAAATTGCTAG

CviRI	FauI	Tsp509I	AciI	Cac8I	TaiI	HhaI	ThaI
-------	------	---------	------	-------	------	------	------

AGTTCCCGATGCAGATATTCTGAATTATGCCGGCACAGTCTGGTATCAGCGCGAAGTCT 2340

2281 TCAAGCGGCTACGTCTATAAGCATTAATACGCCGTTGCAGACCATAGTCGGCTTCAGA

Cac8I	BBVI	CviJI	HaeI	HaeIII	MwoI	Fnu4HI	SfaNI	Tsp45I	TaqI	AciI	RleAI
-------	------	-------	------	--------	------	--------	-------	--------	------	------	-------

TTATACCGAAAGGTTGGCAGGCCAGCGTATCGTGTGCCCTTCGATGCCGTACTCATT 2400

2341 AATATGGCTTCCAACCCGTCCGGTCGCATAGCACGACGCCAAAGCTACGCCAGTGAGTA

BceFI	SimI	BccI	HaeIV	Hin4I	BccI	Fnu4HI	SfaNI	TauI	AciI	CviJI
-------	------	------	-------	-------	------	--------	-------	------	------	-------

ACGGCAAAAGTGTGGGTCAATAATCAGGAAGTGTGGAGCATCAGGCCGTATACGCCAT 2460

2401 TGCCGTTCACACCCAGTTATTAGTCCTTCACTACCTCGTAGTCCCGCCATATGCCGT

MaeIII	Tsp45I	CviJI	NciI	ScrFI	MspI	HphI	BsaAI	SnaBI	RsaI	TaiI
--------	--------	-------	------	-------	------	------	-------	-------	------	------

TTGAAGCCGATGTCACGCCGTATGTTATTGCCGGAAAAGTGTACGTATCACCGTTGTG 2520

2461 AACTTCGGCTACAGTGGCATACAATAACGCCCTTACATGCATAGTGGCAAACAC

BceFI	CjePI	BsrI	AcII	MspI	HphI	Bst4CI	CjePI
-------	-------	------	------	------	------	--------	-------

FauI

NciI

ScrFI

CjePI

MspI

BsrI

AcII

HphI

TGAACAAACGAACTGAACTGGCAGACTATCCCGCCGGGATGGTATTACCGACGAAAACG 2580

2521 ACTTGGCTTGACTTGACCGTCTGATAGGGCGGCCCTTACCAACTATGGCTGCTTTGC

BceFI	NlaIII	MseI	MspI	HinfI	TfiI	Fnu4HI	Tsp509I
-------	--------	------	------	-------	------	--------	---------

GCAAGAAAAAGCAGTCTTACTTCCATGATTTCTTAACTATGCCGAATCCATCGCAGCG 2640

2581 CGTTCTTTCGTCAGAATGAAGGTACTAAAGAAATTGATAACGCCCTTAGGTAGCGTCG



# 9/21 REPLACEMENT SHEET

Fig. 1A(cont.)

2641 TAATGCTCTACACCACGGCGAACACCTGGTGGACGATATCACCGTGGTACCGCATGTCTG 2700  
 ATTACCGAGATGTGGTGCCTGTGGACCCACCTGCTATAGTGGCACCACTGCGTACAGC

2701 CGCAAGACTGTAACCACGGCTCTGTTGACTGGCAGGTGGCCATGGTATGTCAGCG 2760  
 GCGTTCTGACATTGGTGCAGACAACTGACCGTCCACCACCGTTACCACTACAGTCGC

2761 TTGAACCTGCGTGATGCGGATCAACAGGTGGTTGCACCTGGACAAGGCAGTAGCGGGACTT 2820  
 AACTTGACGCACTAGCCTAGTTGTCCACCAACGTTGACCTGTTCCGTGATGCCCTGAA

2821 TCGAAAGTGGTGAATCCGACCTCTGGCAACCGGGTGAAGGTTATCTCTATGAACTGTGCG 2880  
 ACGTTACCACTTAGGCGTGGAGACCGTTGGCCACTTCCAATAGAGATACTTGACACGCC

2881 TCACAGCCAAAAGCCAGACAGAGTGTGATATCTACCCGCTTCGCGTCGGCATCCGGTCAG 2940  
 AGTGTGGTTTCGGTCTGTCTCACACTATAGATGGCGAAGCGCAGCCGTAGGCCAGTC

2941 TGGCAGTGAAGGGCGAACAGTTCTGATTAACCACAAACCGTTCTACTTTACTGGCTTTG 3000  
 ACCGTCACCTCCGCTTGTCAAGGACTAATTGGTGTGGCAAGATGAAATGACCGAAAC

3001 GTCGTCATGAAGATGCGGACTTGCGTGGCAAGGATTGATAACGTGCTGATGGTGCACG 3060  
 CAGCACTTCTACGCCTGAACGCACCGTTCTAAGCTATTGCACGACTACCACGTGC

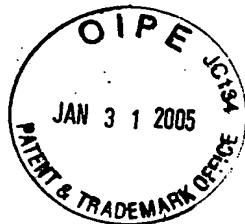


Fig.1A(cont.)

10/21 REPLACEMENT SHEET

3061 *ACCACGCAATTAAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCCTTACG* 3120  
*TGGTGCCTAATTACCTGACCTAACCCGGTTGAGGATGGCATGGAGCGTAATGGGAATGCG*

3121 *CTGAAGAGATGCTCGACTGGCAGATGAACATGGCATCGTGGTATTGATGAAACTGCTG* 3180  
*GACTTCTCTACGAGCTGACCCGTCTACTTGTACCGTAGCACCACTAACTACTTTGACGAC*

3181 *CTGTCGGCTTAACTCTCTTTAGGCATTGGTTCGAAGCGGGCAACAAGCCGAAAGAAC* 3240  
*GACAGCCGAAATTGGAGAGAAATCCGTAACCAAGCTTCGCCCGTTGTCGGCTTCTTG*

3241 *TGTACAGCGAAGAGGGAGTCACGGGGAAACTCAGCAAGCGCACTTACAGGCATTAAAG* 3300  
*ACATGTCGCTTCTCCGTCAAGTTGCCCTTGAGTCGTTCGCGTGAATGTCGCTAATTTC*

3301 *MaeIII Tsp45I HhaI BsaWI BciVI*  
*AluI CviJI MwoI ThaI CjeI BsI I TaqII HphI CjeI*  
*AGCTGATAGCGCGTGACAAAAACCAACCCAAAGCGTGGTATGTGGAGTATTGCCAACGAAC* 3360  
*TCGACTATCGCGACTGTTTTGGTGGTTCGCAACACTACACCTCATAACGGTTGCTTG*

3361 *BscGI BsiHKAI Bsp1286I BsrI EcII TspRI AfI*  
*AciI CviRI ApaLI SspI ThaI HhaI MwoI AfI*  
*CGGATACCCGTCCGCAAGGTGCACGGGAATATTCGCGCCACTGGCGGAAGCAACCGCGTA* 3420  
*GCCTATGGCAGGCAGTCCACGTGCCCTTATAAGCGCGGTGACCGCCTTCGCGCAT*

3421 *DonI HgaI Sau3AI HgaI*  
*SimI TagI AfI HphI ThaI HgaI MluI*  
*AACTCGACCCGACGGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCG* 3480

## REPLACEMENT SHEET

11/21

Fig. 1A (cont.)

JAN 3 1 2005

O I P E  
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P A T E N T & T R A D E M A R K O F F I C E

TTGAGCTGGCTGCCAGGCTAGTGGACGCAGTTACATTACAAGACGCTGCGAGTGTGGC

3481 ATACCATCAGCGATCTCTTGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCC  
TATGGTAGTCGCTAGAGAAACTACACGACACGGACTGGCAATAATGCCCTACCATACAGG 3540

3541 AAAGCGGCATTTGGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGG 3600  
TTTCGCCGCTAACCTTGGCGTCTTCCATGACCTTTCTTGAAGACCGGACCGTCC

3601 AGAAACTGCATCAGCCGATTATCATCACCGAATACGGCGTGGATACGTTAGCCGGCTGC 3660  
TCTTGACGTTAGTCGGCTAATAGTAGTGGTTATGCCGACCTATGCAATCGGCCGACG

3661 ACTCAATGTACACCGACATGTGGAGTGAAGAGTATCAGTGTGCATGGCTGGATATGTATC 3720  
TGAGTTACATGTGGCTGTACACCTCACTTCTCATAGTCACACGTACCGACCTATACATAG

3721 HgAI DpnI ThaI  
ThaI Sau3AI HaeII CjePI ApoI  
AciI BceFI HhaI Tsp509I CjePI  
ACCGCGTCTTGATCGCGTCAGCGCCGTCGTGGTAACAGGTATGGAATTCGGCGATT 3780  
TGGCGCAGAAACTAGCGCAGTCGGCAGCAGGCCACTGTCCATACCTAAAGCGGCTAA

3781 HhaI DpnI AlwI  
ThaI MaeIII BstYI HinfI  
MnlI MwoI AciI Sau3AI NruI  
TTGCGACCTCGCAAGGCATATTGCGCGTTGGCGGTAAACAGAAAGGGATCTCACTCGCG 3840  
AACGCTGGACCGTCCGTATAACGGCAACCGCCATTGTTCTTCCTAGAAGTGACCGC

CviJI



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12/21

Fig.1A(cont.)

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Fnu4HI | CviRI | MwoI |  
 TaeI | Fnu4HI | BspGI | NlaIII |  
 AcII | BbvI | TsaeI | BcgI | Bsrl |  
 BsiEI | | | | |  
 ACCGCAAAACCGAAGTCGGCGGCTTTCTGCTGCAAAAACGCTGGACTGGCATGAACCTCG  
 3841 TGGCGTTGGCTTCAGCCGCCGAAAAGACGACGTTTGCGACCTGACCGTACTTGAAGC 3900

BslI | ScrFI |  
 BcgI | ECORII |  
 Fnu4HI | BcgI |  
 HphI | Tth111II |  
 MnII | HinII |  
 TaeI | TfII |  
 AcII | BbvI |  
 GTGAAAAACCGCAGCAGGGAGGCACAAATGAATCAACAACTCTCCTGGCGCACCATCGT  
 3901 CACTTTTGGCGTCGTCCTCCGTTACTTAGTTGAGAGGACCGCGTAGCA 3950

Tsp509I | NlaIII |  
 RcaI |  
 DpnI |  
 BclI |  
 Sau3AI |  
 KpnI |  
 NlaIV |  
 RsaI |  
 BanI |  
 NciI |  
 ScrFI |  
 SmaI |  
 MspI |  
 NciI |  
 ScrFI |  
 Aval |  
 BsaJI |  
 BanII |  
 BsiHKAI |  
 Bsp1286I |  
 SacI |  
 AluI |  
 CviJI |  
 Tsp509I |  
 Aval |  
 BsaJI |  
 CviJI |  
 SfcI |  
 BcgI |  
 MnII |  
 CGCTACAGCCTCGGAATTGCTACCGAGCTccccgggtacctgatcatgagtaatttagctC  
 3961 GCGATGTCGGAGCCCTAACGATGGCTCGAGggccatggactagactactattaatcgAG 4020

BsiEI | MseI | MspI |  
 Pvul | AfII | BsII |  
 ApoI | DpnI | HinII |  
 Tsp509I | Sau3AI | TfII |  
 GAATTTCGGATCGTTCAACATTTGGCAATAAGTTCTTAGATTGAATCCTGTTGC  
 4021 CTTAAAGGGCTAGCAAGTTGTAAACCGTTATTCAAGAATTCTAACTTAGGACAGCG 4080

AflII | BspLU11I |  
 BspLU11I | MseI |  
 Tsp509I | NlaIII |  
 MseI | TaeI | NspI |  
 MwoI | BsabI | Tsp509I | Tsp509I |  
 CGGTCTTGGATGATTATCATATAATTCTGTTGAAATTACGTTAACGATGTAATAATTAA  
 4091 GCCAGAACGCTACTAATAGTATATTAAAGACAACTTAATGCAATTGCGTACATTATTAA 4140



JAN 31 2005

13/21 REPLACEMENT SHEET

Fig. 1A (cont.)

Fig. 1B

### Enzymes that do cut:

### Enzymes that do not cut:



## REPLACEMENT SHEET

15/21

pGPTV-GUS-kan

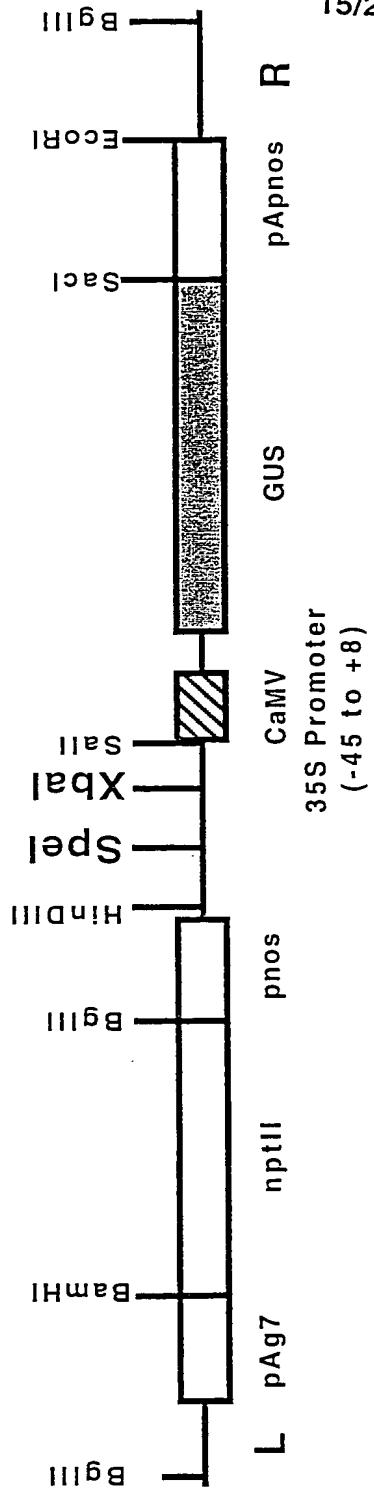


Fig. 3

# REPLACEMENT SHEET

Fig. 4

